WHAT IS CLAIMED IS:

1. A system, comprising:

a system input to receive a quantity of proteomic data obtained from mass spectrometric analysis of a biological sample;

a metadata repository to store a quantity of metadata that includes the quantity of proteomic data;

a rules database to store at least one rule derived from an analysis of the quantity of proteomic data; and

a processor to perform at least one operation or algorithm to effect the analysis of the quantity of proteomic data and thereby derive the at least one rule.

2. The system of claim 1, further comprising a facts database to store a quantity of raw data, to store a quantity of data that is imported from the metadata repository, or both.

3. The system of claim 2, wherein the processor is configured to perform a translation, modification, reorganization, or filtering operation on at least a portion of the quantity of data that is imported from the metadata repository to the facts database.

4. The system of claim 1, further comprising a processes database to store a quantity of processes.

5. The system of claim 4, wherein at least one process included in the quantity of processes is dependent upon the outcome of an analysis of at least one rule stored in the rules database.

6. The system of claim 2, wherein the processor is configured to implement at least one machine learning algorithm to generate at least one soft rule that is stored in the rules database based on an analysis of at least a portion of the quantity of proteomic data, at least a portion of the quantity of metadata, at least a portion of the raw data, at least one rule, or combinations thereof.

7. The system of claim 6, wherein the at least one soft rule explains a clinically relevant variation in at least a portion of the proteomic data.

8. The system of claim 1, further comprising a support vector machine, comprising:

a covariance matrix to maintain information about closeness of relationships in aspects of proteomic data from biological samples stored in the metadata repository; and

a covariance database,

wherein the system is configured to run a suite of kernel principal component analyses on the covariance matrix to run the support vector machine.

9. The system of claim 1, further comprising a secondary system input to receive a quantity of input data from a source selected from the group consisting of a medical or research instrument, a system user, an external database, and combinations thereof.

10. The system of claim 1, further comprising a system output.

11. The system of claim 2, wherein the quantity of metadata, the raw data, or both include patient information, clinical information, or both.

12. The system of claim 1, further comprising a metadata curation tool to browse and maintain the metadata.

13. The system of claim 4, further comprising a common data element maintenance and electronic data capture feature.

14. The system of claim 13, wherein the common data element maintenance and electronic data capture feature further comprises:

a form authoring tool to create at least one form; and

a render agent to render the at least one form in various formats,

wherein the processor is configured to execute instructions of the form authoring tool and the render agent, and the at least one form is stored in the processes database.

15. The system of claim 14, wherein the common data element and electronic data capture feature further comprises an additional component selected from the group consisting of a repository security system to enable the restriction of access to the metadata, a data archival facility to maintain the metadata, a backup and recovery system to enable the restoration of the metadata in the event of a catastrophic event, a repository accounting

system to monitor access and changes to the metadata, a data transfer system to facilitate data transport, and combinations thereof.

16. The system of claim 10, further comprising an automated clinical trial visit scheduler to schedule visits and procedures to be performed during a patient visit.

17. The system of claim 2, further comprising an electronic medical records translator to translate at least one item of metadata into at least one fact.

18. The system of claim 1, wherein said biological sample is selected from the group consisting of a body fluid, blood, serum, spinal fluid, urine, sweat, saliva, tears, breast aspirate, prostate fluid, seminal fluid, stool, cervical scraping, cytes, amniotic fluid, intraocular fluid, mucous, moisture in breath, animal tissue, cell lysates, tumor tissue, hair, skin, buccal scrapings, nails, bone marrow, cartilage, prions, bone powder, and ear wax.

19. The system of claim 1, wherein the mass spectrometric analysis comprises a Fourier transform mass spectrometric analysis.

20. A method for identifying a rule that explains a clinically relevant variation in proteomic data obtained from multiple sources, comprising:

providing a system, comprising:

a system input to receive a quantity of proteomic data obtained from mass spectrometric analyses of multiple biological samples,

a metadata repository to store a quantity of metadata that includes the quantity of proteomic data,

a rules database to store at least one rule derived from an analysis of the quantity of proteomic data, and

a processor to perform at least one operation or algorithm to derive the at least one rule;

performing at least one operation or algorithm to analyze at least a portion of the quantity of proteomic data, at least a portion of the quantity of metadata, at least one rule, or combinations thereof; and

deriving a rule that explains a clinically relevant variation from the at least one operation or algorithm.

21. The method of claim 20, wherein the at least one operation or algorithm includes at least one machine learning algorithm.

22. The method of claim 21, wherein the system further comprises a support vector machine, comprising:

a covariance matrix to maintain information about closeness of relationships in aspects of at least a portion of the quantity of proteomic data from multiple biological samples; and

a covariance database,

wherein the method further comprises running a suite of kernel principal component analyses on the covariance matrix to run the support vector machine.